

PROTEOMIC DETERMINATION OF PROTEIN NITROTYROSINE MODIFICATIONS
USING MASS SPECTROMETRY

ABSTRACT OF THE DISCLOSURE

Compositions and methods are provided for identifying oxidative modifications of proteins by mass spectrometric analysis, including MALDI-TOF MS, of protein and peptide fractions of biological samples to determine specific occurrences of nitrotyrosine at amino acid sequence and proteomic levels. Diagnostic methods for diseases characterized by elevated free radicals and oxidative stress, and screening assays for therapeutic agents useful in treating such diseases, are also disclosed.